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1653

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/509,994

DATE: 11/08/2001
 TIME: 12:22:23

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3 <110> APPLICANT: YUI, MASAKI
 4 YOKOZAWA, AKIRA
 5 MURATA, TOMOYO
 6 TSURUTA, KAZUHISA
 7 SHIMIZU, HIROTOMO
 9 <120> TITLE OF INVENTION: METHOD FOR KEEPING THE QUALITY OF AQUEOUS PARENTERAL
 10 SOLUTION OF THROMBOMODULIN IN STORAGE AND DISTRIBUTION
 12 <130> FILE REFERENCE: KP-8753
 14 <140> CURRENT APPLICATION NUMBER: 09/509,994
 15 <141> CURRENT FILING DATE: 2000-05-08
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04609
 18 <151> PRIOR FILING DATE: 1998-10-13
 20 <150> PRIOR APPLICATION NUMBER: JP 9-281659
 21 <151> PRIOR FILING DATE: 1997-10-15
 23 <150> PRIOR APPLICATION NUMBER: JP 9-308523
 24 <151> PRIOR FILING DATE: 1997-11-11
 26 <160> NUMBER OF SEQ ID NOS: 6
 28 <170> SOFTWARE: PatentIn Ver. 2.1
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 516
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: Partial amino acid sequences of a human
 37 thrombomodulin
 39 <400> SEQUENCE: 1
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 41 1 5 10 15
 43 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
 44 20 25 30
 46 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
 47 35 40 45
 49 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
 50 50 55 60
 52 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
 53 65 70 75 80
 55 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
 56 85 90 95
 58 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
 59 100 105 110
 61 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
 62 115 120 125
 64 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
 65 130 135 140
 67 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
 68 145 150 155 160
 70 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg

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71          165          170          175
73 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr
74          180          185          190
76 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
77          195          200          205
79 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
80          210          215          220
82 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
83 225          230          235          240
85 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
86          245          250          255
88 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
89          260          265          270
91 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
92          275          280          285
94 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
95          290          295          300
97 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
98 305          310          315          320
100 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
101          325          330          335
103 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
104          340          345          350
106 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
107          355          360          365
109 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
110          370          375          380
112 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
113 385          390          395          400
115 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
116          405          410          415
118 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
119          420          425          430
121 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
122          435          440          445
124 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
125          450          455          460
127 Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile Gly Thr Asp Cys
128 465          470          475          480
130 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
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136 Val His Ser Gly
137          515
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 516
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens

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145 <220> FEATURE:

146 <223> OTHER INFORMATION: Partial amino acid sequences of a human
147 thrombomodulin

149 <400> SEQUENCE: 2

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150 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
151   1       5       10       15
153 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
154       20       25       30
156 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
157       35       40       45
159 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
160       50       55       60
162 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
163   65       70       75       80
165 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
166       85       90       95
168 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
169       100      105      110
171 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
172       115      120      125
174 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
175       130      135      140
177 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
178 145       150      155      160
180 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
181       165      170      175
183 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr
184       180      185      190
186 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
187       195      200      205
189 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
190       210      215      220
192 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
193 225       230      235      240
195 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
196       245      250      255
198 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
199       260      265      270
201 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
202       275      280      285
204 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
205       290      295      300
207 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
208 305       310      315      320
210 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
211       325      330      335
213 Pro Gln Arg Cys Val Asn Thr Gln Gly Phe Glu Cys His Cys Tyr
214       340      345      350
216 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro

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217          355          360          365
219 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
220          370          375          380
222 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
223 385          390          395          400
225 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
226          405          410          415
228 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
229          420          425          430
231 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
232          435          440          445
234 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
235          450          455          460
237 Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile Gly Thr Asp Cys
238 465          470          475          480
240 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
241          485          490          495
243 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
244          500          505          510
246 Val His Ser Gly
247          515

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250 <210> SEQ ID NO: 3

251 <211> LENGTH: 1548

252 <212> TYPE: DNA

253 <213> ORGANISM: Homo sapiens

255 <220> FEATURE:

256 <223> OTHER INFORMATION: Partial base sequences of a human thrombomodulin
 257 gene

259 <400> SEQUENCE: 3

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261 gcagagccgc agccgggtgg cagccagtgc gtcgagcacg actgcttcgc gctctaccgc 120
262 ggccccgcga ccttcctcaa tgccagtcag atctgcgacg gactgcgggg ccacctaatg 180
263 acagtgcgct cctcggtggtc tgccgatgtc atttccttgc tactgaacgg cgacggcggc 240
264 gttggccgcc ggcgctcttg gatcggcctg cagctgccac ccggtgcgg cgacccaag 300
265 cgctcggggc cctgcgcggg cttccagtgg gttacgggag acaacaacac cagctatagc 360
266 aggtgggcac ggctcgacct caatggggct cccctctgcg gccggttggt cgtcgtctgc 420
267 tccgctgctg aggccactgt gccagcgag ccgatctggg aggagcagca gtgcgaagtg 480
268 aaggccgatg gcttcctctg cgagtccac ttcccagcca cctgcaggcc actggctgtg 540
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270 ggagcggact tccaggcgct gccggtgggc agctccgccc cggtgggtcc cctcggctta 660
271 cagctaattg gcaccgcgcc gcccggagcg gtccaggggc actgggccaag ggaggcgcgc 720
272 ggcgcttggt actgcagcgt ggagaaacgg ggctgcgagc acgcgtgcaa tgcgatccct 780
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280 ccgcacaggt gccagatggt ttgcaaccag actgcctgtc cagccgactg cgaccccaac 1260
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282 gacatcgacg agtgcgaaaa cggcggttcc tgctccgggg tgtgccacaa cctccccggt 1380
283 accttcgagt gcatctgcgg gcccgactcg gcccttgccc gccacattgg caccgactgt 1440
284 gactccggca aggtggacgg tggcgacagc ggctctggcg agcccccgcc cagcccgacg 1500
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289 <211> LENGTH: 1548
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Partial base sequences of a human thrombomodulin
295 gene
297 <400> SEQUENCE: 4
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321 accttcgagt gcatctgcgg gcccgactcg gcccttgccc gccacattgg caccgactgt 1440
322 gactccggca aggtggacgg tggcgacagc ggctctggcg agcccccgcc cagcccgacg 1500
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327 <211> LENGTH: 21
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
333 peptide
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Synthetic DNA for mutation

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VERIFICATION SUMMARY

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